TTCTGTAAGAATCAATTGTCTATATGGAATTTAGGATAAAGAATATI TTCTGTAAGAATCAATTGTCTATATGGAATTTAGGATAAAGAATATT TTCTGTAAGAATCAATTGTCTATATGGAATTTAGGATAAAGAATATT TTCTGTAAAAAAGAGTTATTATTATTATTATTGTGCAACAAAAA TCTGTAAAAATTTATACACAGAAAATTAACAAAAAATCTGTAAGAA TCTGTAAAATTTATACACACAAAAATTAACAAAAAATCTGTAAGAA TGGGAATTTAGGATATCTACAAAAATTAACAAAAGATTAACAATAAAA TGGAAATTTAGGATATTTACAATAAAAAAAATTAACAATAAAA	HS28H20 127418 bp DNA PRI Human DNA sequence from clone RP1-28H20 on chromo Contains the SLC2A10 gene encoding a solute carri (facilitated glucose transporter) member 10, the gene, ESTs, STSs, GSSs and three CpG islands, compact CpG island	Ramsay, H. Direct Submission Submitted (18-APR-2001) Sanger Centre, Hinxton, CB10 15A, UK. E-mail enquiries: humquery@sanger.ecuk requests: clonerequest@sanger.ac.uk on Mar 7, 1999 this sequence version replaced git buring sequence assembly data is compared from on Where differences are found these are annotated tromy wariation annotation may not be found in the sequence are annotated to variation annotation may not be found in the sequences are annotated at together with a note of the overlapping clone nan variation annotation may not be found in the sequence corresponding to the overlapping clone, as we sufform a small overlap as described above. The following abbreviations are used to associate	numbers given in the feature table with their sou Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORN on the WORWEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpe was generated from part of bacterial clone contiguans generated from part of bacterial clone contiguans generated from part of bacterial clone contiguans physical properties. Further information can be found http://www.sanger.ac.uk/Rep/Chr20 This sequence is the entire insart of clone RP1: was finished as follows unless otherwise noted: either double-stranded or sequenced with an alter covered by high quality data (i.e., phred quality attempt was made to resolve all sequencing proble compressions and repeats; all regions were covered by as unconfirmed by restriction dieser. RP1-28H20 is was confirmed by restriction dieser.	RPCI-1 constructed by the group of Pieter de Jondetails see http://www.chori.org/bacpac/home.htm VECTOR: pCYPAC2. Location/Qualifiers 1. 127418 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="20" /clone="RPI-28H20" /clone="RPI-28H20" /clone="RPI-28H20" /clone="RPI-28H20" /clone="Ib="RPCI-1" complement(join(<1. :562,2463. :3110))
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ttgta 3120 17GTA 2880 17GTA 2880 1161 17GTA 2940 17GCT 3240 1161 17GCT 3240 17GCT 3240 17GCT 3240			28 28 28 28 28 28 28 28 28 28 28 28 28 2	grgcc 4020 1 Grgcc 4020 1 1 1 1 1
ttacccaggtccctcttggacctgta TTALCINIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	agatotrocttgatcong agatotrocttgatcong AGATOTTCOTTGTATCONG ggttgctacatttcaggattt 	actcttatggagacctaggggag 	GCGGGATAAATGCCGGTGAGG GCGGATAAATGCCGGTAATG GCGGATAAATGCCGGTAAA ACATGGTGTATAGCACCAAAA CCGTTCCAGCGACGAGG 	acctatacccattcttcagtgcc
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	Eatctt 	gaggctattcct 		ycat
ggaaatttctacttat 				Accasasttca
999cct99 [11111] 396ccT666 991ca999 [11111] 367cA666 [11111] A666ACT6 A666ACT6 CCCT99atc	CCCGGC CCCGGC CTGGC CTGCTG IIIII AAGTT FACAT	######################################	1 2 3 3 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	tgtaat 11111 16111 11111 11111 Cagts Cagts Cagts
3061 ccar 1 1 1 1 2821 CCAA 3121 aag 3121 aag 3181 ggar 1 1 1 1 1 1 1 1 1 1	301 act 100 ac	541 c 301 C 601 a 361 A 421 b	3721 tgati 3481 TGAT 3781 CAAA 3841 ALGAA 3601 ALGG 3901 AAGG 1115	3961 tag 111 3721 TAG 4021 tag 3781 TAG 4081 tcg 4081 tcg 111 111 111 114 114 114 114 11
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**UK/Projects/C_elegans/wormpep This sequence art of bacterial clone contigs of human ructed by the Sanger Centre Chromosome 20 her information can be found at.

**UK/MEP/Chr20

ows unless otherwise noted: all regions were entire insert of clone RPI-28H20 This sequence ows unless otherwise noted: all regions were entire insert of clone RPI-28H20 This sequence ows unless otherwise noted: all regions were estimated (i.e., phred quality >= 30); an resolve all sequencing problems, such as estels; all regions were covered by at least one more than one MI3 subclone; and the assembly triction digest. RPI-28H20 is from the library y the group of Pieter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y data is compared from overlapping clones. ound these are annotated as variations the overlapping clone name. Note that the y not be found in the sequence submission talapping clone, as we submit sequences with described above.
                                                                                                                                                                                                                                                                                                                                                                                                          cione RP1-28H20 on chromosome 20q13.1 tenceding a solute carrier family 2 misporter) member 10, the 5' end of a novel and three CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          data; Craniata; Vertebrata; Euteleostomi;
nates; Catarrhini; Hominidae; Homo.
                                                             ttgtaagttgtgtgcaacaaacatacctttatc 4260
                                                                                                                                              Sanger Centre, Hinxton, Cambridgeshire, quiries: humquery@sanger.ac.uk Clone
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Jence version replaced gl:4056528.
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n:9606"
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Anotes LTRIEC repeat: matches 126. .316 of consensus 10631. .10690
Anotes MITID repeat: matches 445. .505 of consensus 10691. .10995
Anotes MITID repeat: matches 1. .295 of consensus 10996. .11200
Anotes MITID repeat: matches 248. .445 of consensus 11232. .11634
Anotes MITID repeat: matches 248. .445 of consensus 11232. .11634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="FAM repeat: matches -126. .41 of consensus". 19258. .19336
/note="MER57-internal repeat: matches 7168. .7244 of
                                                                                                                                                                                                                                                                                                  11670. 11761

//note="MLTID repeat: matches 128. 192 of consensus"

11762. 12062

//note="AllSx repeat: matches 1. 293 of consensus"

12063. 12180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13210. .1332

/note-"MER20 repeat: matches 1. .215 of consensus"

/note-"MIR repeat: matches 104. .146 of consensus"

/note-"MIR repeat: matches 330. .452 of consensus"

/note-"LTR33 repeat: matches 330. .452 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8774. .15952
note="MER58A repeat: matches 42. .220 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"MLT1J repeat: matches 252. .368 of consensus"
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Anote-"AluJb repeat: matches 1. .296 of consensus" 16600. .16635
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/note="MER53 repeat: matches 2. .180 of consensus"
19721. .20190
/note="LTR8 repeat: matches 251. .691 of consensus"
20238. .20493
/note="LTR8 repeat: matches 1. .256 of consensus"
20704. .20978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3894. .14254
'note="12 repeat: matches 2255. .2619 of consensus"
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// Anote = 12 repeat: matches 2617. .2748 of consensus = 14446. .14525

// Anote = 4 copies 20 mer 76% conserved = 15752

// Anote = AluJb repeat: matches 2. .278 of consensus = 15752
                                        /note="AluJo repeat: matches 74. .306 of consensus"
10038. .10206
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/note="LTR26 repeat: matches 246. .553 of consensus complement(18333. 18408)
                 repeat: matches 2170. .2303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLTID repeat: matches 1, .128 of consensus" complement(12181, .12344)
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note="47 copies 2 mer ta 70% conserved"
7559. 17868
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3011. .13129
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FVDYASNCLYMEBIBGSVTVRDY IQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIH
GDLTTSNMLLKPPLEQLNIVLIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVF
/gene="dJ101A2.2"
//note="match: cDNAs: Em:AK013049 Em:AK011574
/note="match: cDNAs: Em:AK033726 Em:T87841 Em:AK56018 Em:AA513277
Em:AA985248 Em:AA680750 Em:AA6461487 Em:AI028588
Em:AA659710 Em:AX149891 Em:AA579641 Em:AA516077
Em:AA60132 Em:AA483490 Em:AA378651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'translation-"MAAARATTPADGEEPAPEAEALAAARERSSRFLSGLELVKQGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6270 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669. 5895
note="LIME repeat: matches 5501. 5739 of consensus"
332. 6548
note="L2 repeat: matches 2524. 2746 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .391 of consensus"
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'note-"MLT11 repeat: matches 311. .382 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323. .7417 '
note="L2 repeat: matches 2389. .2513 of consensus"
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note-"MLT1J repeat: matches 9. .211.of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"MIR repeat: matches 102. .242 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626. .6915
note="AluSx repeat: matches 3. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               023. 7322
note-"AluJo repeat: matches 1. .312 of consensus"
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note="MIR repeat: matches 93. .262 of consensus"

    1145
    10te="AluSx repeat: matches 1. ,298 of consensus"

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hote-"MER94 repeat: matches 1. .62 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 33. .135 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"MIR repeat: matches 8. .135 of consensus"
                                                                                                                                                                                                                                                                                                           /note="supported by FGENESH and GENSCAN
continues in Em:AL133520 as dJ101A2.2"
                                                                                                                                                                                                                               /note="match: STS: Em:HS28H20T"
complement(join(84. .562,2463. .2745))
/gene="dJ101A2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="3 copies 20 mer 85% conserved"
omplement(2876. .3110)
gene="dJ101A2.2"
                                                                                                                                                                                                                                                                                                                                                                       /evidence-not_experimental
/product="dJ28H20.2 (novel protein)"
/protein_id="CAC00561.1"
/db_xref="GI:9588402"
                                                                                                                          /evidence-not_experimental
/product-"dJ28H20.2 (novel protein)"
complement(1. .3110)
/gene-"dJ101A2.2"
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note="LIMA8 repeat: matches 4532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 33.
155. .2248
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note="CpG island"
evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:Q9NQE6".
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Query Match Best Local Similarity	41.2%; Score 1810; DB 9 99.9%; Pred. No. 0;	70 - -	Db 48787	
Conser	ervative 0; Mismatches 2; Indels 0; Gaps 0;		0 0 0	THEFT
JCTAAT	acccagctaatttattttagcagagatgggtttcactgtgttggccaggctggtcgtg 2535 		o 1	TTGAGGC
otgago! 	2595		Qy 3616 Db 48907	tectgati TCCTGAT
actetti 	26		QY 3676 Db 48967	gtgtttt GGGTTTT
caccago: { CACCAGO	.27		Qy 3736 Db 49027	tgatttt
cattgctd 	gtgtcattgctgtaggaatgaccacgggcctcagtttccccatttgtataatgggaagcc 2775 	, <u>38</u>	Oy 3796 Db 49087	ágtátgto AGTATGTO
ccaggtc: 	28 4		Oy 3856 Db 49147	ttccagta TTCCAGTA
ggagetgt GGAGCTG1	289		Oy 3916 Db 49207	gagttete GAGTTETE
acaaacct ACAAACC1	gccaacaaactgcttgtcaatattgcctttgcctcttggcagcccttgaacttgagtaa 2955 {		Oy 3976 Db 49267	tttcaacc TTCAACC
CAACTCCC	u, 4+	·	Oy 4036 Db 49327	cagggatt CAGGGATI
tatttage 	ggtatatttagaccctgtttcctttcaggagggtcccagctggtccagggcctgggaaa 3075 		Oy 4096 Db 49387	actttgga ACTTTGGA
tacttate TACTTATE	tttctacttatcctcattacccaggtccctcctttggaccctgtaaagggtcagggtgaa 3135 		Oy 4156 Db 49447	ttggctat TTGTCTAT
atggggga 	tcagatgggggactgagcaagtagctatgactgcagatcatgtaaggaagg		Oy 4216 Db 49507	tttattat TTATTAT
ctcccage 	3255	<u>-</u>	Oy 4276 Db 49567	Cacacaaa
atccatgo	gtcatccatgcgtgcacatatgggtgctggcagagcccccaaggactctggcctctcga 3315 		Oy 4336 Db 49627	aatatta AATATTTA
tectatet 	gttetectatettetecattetagatgetteeettgtateeagtgatgtgetggagetgg 3375 		RESULT 5 AX150151/c LOCUS	
gccaaget 	cttigccaagetigtgagagetggtigctacatticaggattittacaagtiggtaaac 3435 	·	DEFINITION ACCESSION VERSION KEYWORDS	
ccattata 	acagccattataaaaaattaaatgatttaaatttataattaagtaaattacattacattacattacataca	· · · · · · · · · · · · · · · · · · ·	SOURCE ORGANISM	human. Homo s Eukary Mammal
attatac	aaaaaattatactcaaaaattcattacttaattitactacctgttactattatctgtgctt 3555	 ,-	REFERENCE AUTHORS	1 (ba Kroes,

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Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; lia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 48966 49026 49326 49386 3915 4035 4095 3795 3855 08-JUN-2001 cttgtttgtagcdatacatggtgtatagcaccaaaaaatggagggattattc PAT 151 385 bp DNA nice 126 from Patent W00136685. 151.1 GI:14348179 sapiens

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uc76f10.xl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1431595 3', mRNA sequence.
                                                                          Length 1049;
                                                                     DB 11;
                                                                                        .3e-77
                                                                                                            0; Mismatches
                                                                   Score 574.6;
Pred. No. 7.3
                                                                   13.1%;
88.7%;
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/note-Torgan: liver; vector: pME18S-FL3; Site_1: Draili (CACTOTOTO); ste_2: Draili (CACTOTOTO); lst strand cDNA was primed with an oligo(df) primer (ATGTGGCCTTTTTTTTTTTTTT) double-stranded cDNA was ligated to a Draili adaptor (TGTTGGCCTACTGG), digested and cloned into distinct braili sites of the pWE18S-FL3 vector (S' site CACTOTGTG, 3' site CACATOTG). About be used to isolate the CDNA insert. Size selection was
                                                1 (bases 1 to 563)
Marta,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CTACTGCTCTAAAAGCTGCG and 3' end
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3816 aatacatggtgtatagcaccaaaaaatggaggattattctccagtagttgaacactgt 3875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attgttttacttttgtcttcctcactagtgtaaacaaaaatttcaaccagcattcatgcc 3995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 AATACATGGTGTATAGCACCAAAAATGGAGGGATTATTCTTCCAGTAGTTGAACACTGT
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                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyRouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 631
Tel: 314 286 1810
Emx: 314 286 1810
Emxil: mouseest@watson.wustl.edu
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/clone="IMAGE:1431595"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="bH108"
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Pred. No. 7.6e-73;
0; Mismatches 3;
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Location/Qualiflers
1. 563
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Best Local Similarity 99.5%;
Matches 550; Conservative
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Length 528;

Score 526.4; DB 10;

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Query Match
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1 (bases 1 to 528)

Hilliar, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

Upubliahed (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 464.
                                                                                                                                                                                                                                                                                                                                                AA4U4352 528 bp mRNA EST 16-MAY-1997
ZV63f10.s1 Soares_totel_ferus_Nb2HF8_9w Home sapiens cDNA clone
IMAGE:758347 3', mRNA sequence.
                                                                         attotytaagaattaattggotatatggaatttaggatagaatattacaataaagagta 4355
                                                                                                                                     4116 caaaaaaaaaatattaacaaaatattctgtaagaatcaattggctatatggaatttagg 4175
                                             263 CAAAAAAAAAAATATTAACAAAATATTCTGTAAGAATCAATTGTCTATATGGAATTTAGG 204
                                                                                                                                                                143 GTGTGCAACAACATACCCTTTATCTCTGTAAATTTATACACACAAAAATTAACAAAAG 84
                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758347"
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1648 Std Error: 0.00
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cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
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ov82b10.x1 Soares_testis_NHT Homo sapiens CDNA clone IMAGE:1643803
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                                                                                                                                                  3925 catteatitteatigiittaetitigietteeteeteagigiaaacaaaaatiteaacea 3984
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High quality sequence stop: 444.
                Pred. No. 1.4e-69;
                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Homo sapiens"
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12.0%;
99.8%;
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Unpublished (1997)
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AIO41537
                                        Matches 527; Conservative
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